IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:
HANNA *et al.*
Appl. No. 09/030,832
Filed: February 26, 1998
For: **$GABA_A$ Receptor Epsilon Subunits**

Art Unit: 1646
Examiner: Landsman, R.
Atty. Docket: 1488.0950001/EKS/KKV

#17
KO
10-11-00

Declaration of Ewen F. Kirkness and Michael C. Hanna Under 37 C.F.R. § 1.131

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

We, Ewen F. Kirkness and Michael C. Hanna hereby declare and state as follows:

1. We are named inventors of the captioned application. This declaration is made to establish completion of the claimed invention in the United States at a date prior to March 8, 1997, the earliest effective date of Garret *et al.*, *J. Neurochem. 68*:1382-1389 (1997) (hereinafter "Garret *et al.*").

2. As much of the claimed invention that is disclosed in Garret *et al.* was completed in this country before March 8, 1997. The following is provided as evidence to such completion. Before March 8, 1997, we identified a human DNA sequence which we understood to encode a novel $GABA_A$ receptor subunit, which we designated as the epsilon subunit. Exhibit A consists of a copy of a notebook page which provides the basis for the foregoing demonstration. The date which has been redacted from Exhibit A is prior to March 8, 1997.

Also before March 8, 1997, we possessed a nucleotide sequence having the designation GRE #5.seq, with a coding region identical to the coding region from nucleotides 41 to 1561 in SEQ ID NO:41 of the captioned application, and which encodes amino acids -18 to 488 in SEQ ID NO:42 of the captioned application. Exhibit B consists of a copy of a notebook page disclosing the nucleotide sequence which provides the basis for the foregoing demonstration. The date which has been redacted from Exhibit B is prior to March 8, 1997.

3. As the persons signing below:

We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patents issued thereupon.

09/25/00
Date

Ewen F. Kirkness

Date

Michael C. Hanna

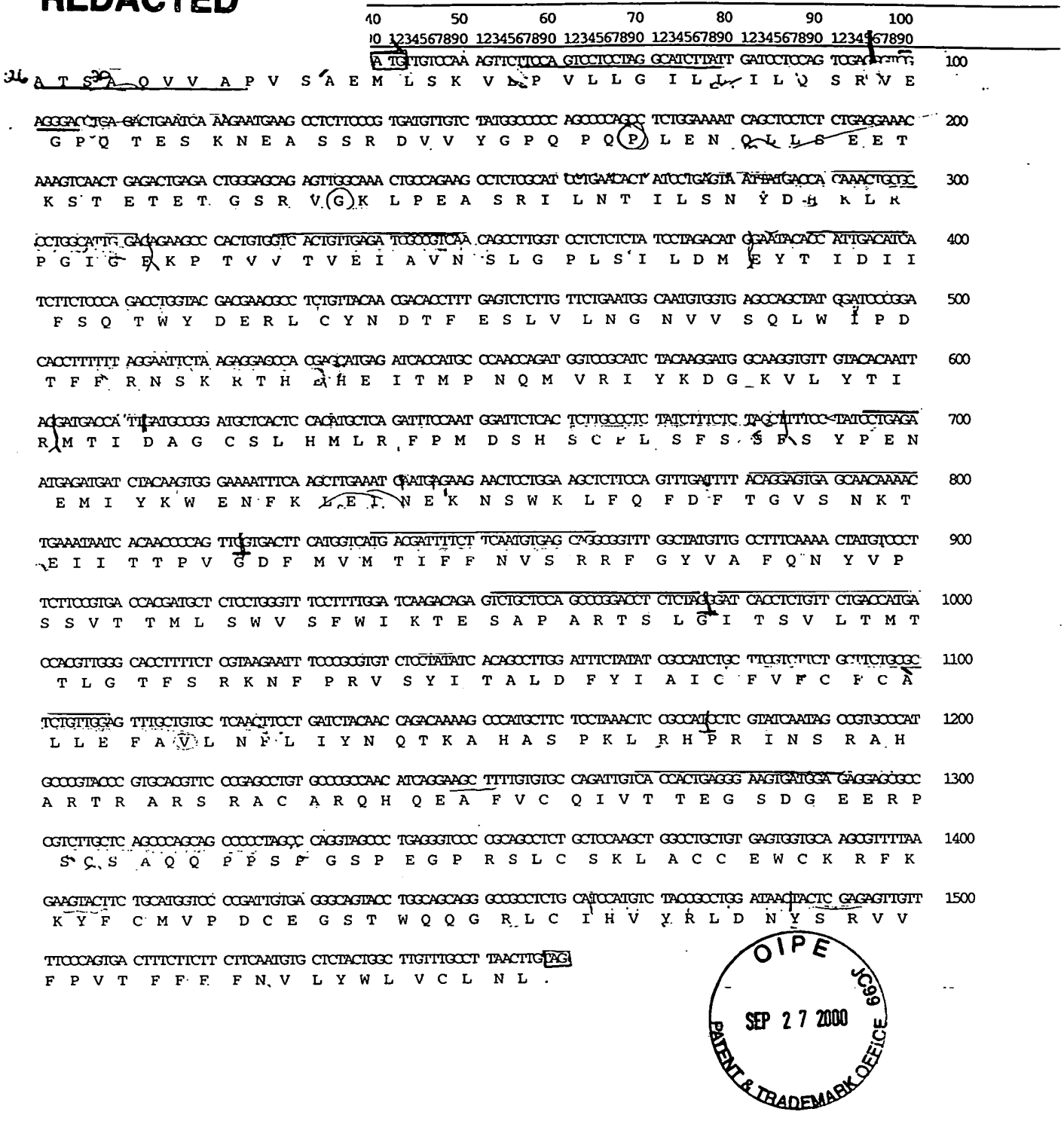
A tblastn search of GenBank (release 89) with GRP.pep hit a human EST sequence that appears to encode a novel GABA-A receptor subunit.

The novel subunit is christened the first epsilon subunit (GRE).

Exhibit B
09/030,832

GRE#5.seq Sequence

REDACTED



OIPE
SEP 27 2000
PATENT & TRADEMARK OFFICE 2900

Due Date: None

Applicants: Hanna *et al.*

Art Unit: 1801

Examiner: to be assigned

Application No.: 09/030,832

Docket: 1488.0950001

Filed: February 26, 1998

Atty: EKS/SGW

For: **$GABA_A$ Receptor Epsilon Subunits**

When receipt stamp is placed hereon, the USPTO acknowledges receipt of the following documents:

1. Transmittal letter (in duplicate); 2. Information Disclosure Statement; 3. Form PTO-1449 (20 pages); and 4. Copies of references AL1, AR1, AS1, AT1, AR2, AS2, AT2, AR3, AS3, AT3, AR4, AS4, AT4, AR5, AS5, AT5, AR6, AS6, AT6, AR7, AS7, AT7, AR8, AS8, AT8, AR9, AS9, AT9, AR10, AS10, AT10, AR11, AS11, AT11, AR12, AS12, AT12, AR13, AS13, AT13, AR14, AS14, AT14, AR15, AS15, AT15, AR16, AS16, AT16, AR17, AS17, AT17, AR18, AS18, AT18, AR19, AS19, AT19, AR20, and AS20.

Please Date Stamp And Return To Our Courier

NCBI **Sequence revision history** Entrez ?

Revision History for Accession = R07883	
gi	*Update Date*
159806	04/06/95

This sequence was released by NCBI on 04/06/95

Disclaimer

NCBI Entrez Nucleotide QUERY BLAST Entrez2 ?

Other Formats: FASTA Graphic

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LOCUS       R07883         317 bp    mRNA            EST       05-APR-1995
DEFINITION  yf16g04.s1 Homo sapiens cDNA clone 127062 3' similar to
            SP:GAC4_CHICK P34904 GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-4
            SUBUNIT PRECURSOR ;.
ACCESSION   R07883
NID         g759806
KEYWORDS    EST.
SOURCE      human clone=127062 library=Soares fetal liver spleen 1NFLS
            vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B
            (ampicillin resistant) primer=-21m13 Rsite1=Pac I Rsite2=Eco RI
            Liver and spleen from a 20 week-post conception male fetus. 1st
            strand cDNA was primed with a Pac I - oligo(dT) primer [5'
            AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
            I and cloned into the Pac I and Eco RI sites of the modified pT7T3
            vector.  Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 317)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence stops: 241
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1..317
                     /organism="Homo sapiens"
                     /clone="127062"
BASE COUNT       98 a      64 c      91 g      57 t       7 others
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       61 agacgaagca gatggcgata tagaaatcca aggctgtgat ataggagaca cgcgggaaat
      121 tcttacgaga aaaggtnccc aacgtggtca tggtcagaac agaggtgatc cctagagagg
      181 tccgggctgg agcagactct gtcttgatcc naaaaggaaa cccagggaga gcatcgtggg
      241 tcacggaaga ngggacatag ttttgaaagg caccatagcc aaanccgcct nctcacattt
      301 gaggaanttc gtcattg
//
```

Save the above report in Macintosh Text format.

>gb|R07883|R07883 yf16g04.s1 Homo sapiens cDNA clone 127062 3' similar to SP:GAC4_CHICK P34904 GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-4 SUBUNIT PRECURSOR ;.
Length = 317

Minus Strand HSPs:

Score = 622 (171.9 bits), Expect = 5.1e-63, Sum P(4) = 5.1e-63
Identities = 130/138 (94%), Positives = 130/138 (94%), Strand = Minus / Plus

```
Query:  4096 GGCTGTGATATAGGAGACACGCGGGAAATTCTTACGAGAAAAGGTGCCCAACGTGGTCAT 4037
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct:    92 GGCTGTGATATAGGAGACACGCGGGAAATTCTTACGAGAAAAGGTNCCCAACGTGGTCAT 151

Query:  4036 GGTCAGAACAGAGGTGATCCCTAGAGAGGTCCGGGCTGGAGCAGACTCTGTCTTGATCCA 3977
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   152 GGTCAGAACAGAGGTGATCCCTAGAGAGGTCCGGGCTGGAGCAGACTCTGTCTTGATCCN 211

Query:  3976 AAAGGAAACCCAGGAGAG 3959
              ||| | || ||  | |||
Sbjct:   212 AAAAGGAAACCCAGGGAG 229
```

Score = 212 (58.6 bits), Expect = 5.1e-63, Sum P(4) = 5.1e-63
Identities = 44/47 (93%), Positives = 44/47 (93%), Strand = Minus / Plus

```
Query:  3952 GGTCACGGAAGAAGGGACATAGTTTTGAAAGGCAACATAGCCAAACC 3906
             |||||||||||| |||||||||||||||||||| |||||||||| |
Sbjct:   239 GGTCACGGAAGANGGGACATAGTTTTGAAAGGCACCATAGCCAAANC 285
```

Score = 90 (24.9 bits), Expect = 5.1e-63, Sum P(4) = 5.1e-63
Identities = 22/27 (81%), Positives = 22/27 (81%), Strand = Minus / Plus

```
Query:  3977 AAAAGGAAACCCAGGAGAGCATCGTGG 3951
              ||| | || ||  ||||||||||||||
Sbjct:   213 AAAGGAAACCCAGGGAGAGCATCGTGG 239
```

Score = 88 (24.3 bits), Expect = 5.1e-63, Sum P(4) = 5.1e-63
Identities = 22/29 (75%), Positives = 22/29 (75%), Strand = Minus / Plus

```
Query:  3912 CCAAACCGCCTGCTCACATTGAAGAAAAT 3884
             | || |||||| ||||||||  || || |
Sbjct:   280 CAAANCCGCCTNCTCACATTTGAGGAANT 308
```

NCBI **Sequence revision history** Entrez ?

Revision History for Accession = R07942	
gi	*Update Date*
159862	04/06/95

This sequence was released by NCBI on 04/06/95

Direct Link

NCBI Entrez Nucleotide QUERY BLAST Entrez ?

Other Formats: FASTA Graphic

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LOCUS       R07942          477 bp    mRNA            EST       05-APR-1995
DEFINITION  yf16g04.r1 Homo sapiens cDNA clone 127062 5'.
ACCESSION   R07942
NID         g759865
KEYWORDS    EST.
SOURCE      human clone=127062 library=Soares fetal liver spleen 1NFLS
            vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B
            (ampicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI
            Liver and spleen from a 20 week-post conception male fetus. 1st
            strand cDNA was primed with a Pac I - oligo(dT) primer [5'
            AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
            I and cloned into the Pac I and Eco RI sites of the modified pT7T3
            vector.  Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 477)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence stops: 323
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1..477
                     /organism="Homo sapiens"
                     /clone="127062"
BASE COUNT       92 a    103 c    123 g    151 t      8 others
ORIGIN
        1 tgtaggacag tgaactgaga aggaagctat taagattctg gccttggtta gctctcaact
       61 ggccattggt cttgcagtaa gtctttttc tgggcttctt ctggtcctat ttgtatgtat
      121 tgcattgtca catcatgcct ctatcctagg gaatactgtg agctgaaaaa tgagaccctt
      181 actgttcacg tcctgctaag ggggaccgtc gtgtcagcac tgtaatgcag tgatgttttt
      241 tgtgtctttc aggtgacttc atgggtcatg acgattttct tcaatgtgag cagggcggtt
      301 tgggctatgt tgcctttcaa aactatgtcc ccttcttccc gtgaccacgg atggtctccn
      361 ggggtttccn ttttggancc aagacaggag tctggntcca gccccgggac ctttttaggg
      421 gatcaacnct cgttncggac catggaccac gttgggggna acttttnttc gtaagga
//
```

Save the above report in Macintosh Text format.

>gb|R07942|R07942 yf16g04.r1 Homo sapiens cDNA clone 127062 5'.
Length = 477

Plus Strand HSPs:

Score = 1089 (300.9 bits), Expect = 1.3e-114, Sum P(4) = 1.3e-114
Identities = 221/225 (98%), Positives = 221/225 (98%), Strand = Plus / Plus

```
Query:  3651 GCCTTGGCTTAGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCT 3710
             | | | | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    40 GGCCTTGGTTAGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCT 99

Query:  3711 TCTGGTCCTATTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGT 3770
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   100 TCTGGTCCTATTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGT 159

Query:  3771 GAGCTGAAAAATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCA 3830
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   160 GAGCTGAAAAATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCA 219

Query:  3831 CTGTAATGCAGTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGG 3875
             |||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   220 CTGTAATGCAGTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGG 264
```

Score = 236 (65.2 bits), Expect = 1.3e-114, Sum P(4) = 1.3e-114
Identities = 48/49 (97%), Positives = 48/49 (97%), Strand = Plus / Plus

```
Query:  3611 TGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGCT 3659
             ||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct:     1 TGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGTT 49
```

Score = 159 (43.9 bits), Expect = 1.3e-114, Sum P(4) = 1.3e-114
Identities = 35/39 (89%), Positives = 35/39 (89%), Strand = Plus / Plus

```
Query:  3874 GGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGG 3912
             |||||||||||||||||||||||||||||||  | || |
Sbjct:   264 GGTCATGACGATTTTCTTCAATGTGAGCAGGGCGGTTTG 302
```

Score = 153 (42.3 bits), Expect = 1.3e-114, Sum P(4) = 1.3e-114
Identities = 33/36 (91%), Positives = 33/36 (91%), Strand = Plus / Plus

```
Query:  3906 GGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTT 3941
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Sbjct:   298 GTTTGGGCTATGTTGCCTTTCAAAACTATGTCCCCT 333
```

Doc. Ref. AS17
Appl. No. 09/030,832

NCBI **Sequence revision history** Entrez ?

Revision History for Accession = C17228	
gi	*Update Date*
1571935	06/02/97

This sequence was released by NCBI on 09/29/96

Disclaimer

NCBI Entrez Nucleotide QUERY BLAST Entrez ?

Other Formats: FASTA Graphic

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LOCUS       C17228         293 bp    mRNA            EST       04-SEP-1996
DEFINITION  Human placenta cDNA 5'-end GEN-542A05.
ACCESSION   C17228
NID         g1571935
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone:542A05.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (sites)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE     Otsuka cDNA project
  JOURNAL   Unpublished (1996)
REFERENCE   2  (bases 1 to 293)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES             Location/Qualifiers
     source          1..293
                     /organism="Homo sapiens"
                     /clone="542A05"
                     /tissue_type="placenta"
BASE COUNT       74 a      68 c      81 g      70 t
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       61 ggagcagtgc tcactcacga aggcattttg ccatcacatg aatgtgcaga aaggaggcca
      121 aaagcattct gtgcttctcc accacagcac agacttccct agtctcattt gctgagagta
      181 gacattctga gggccagcag tgcaggtgtg atgtgcctca gagggtatga gcccttagtc
      241 agccatctgg atatcagctg cgtgggcatg atatctagaa ggctaattga ttt
//
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Save the above report in Macintosh Text format.

>gb|C17228|C17228 Human placenta cDNA 5'-end GEN-542A05.
Length = 293

Plus Strand HSPs:

Score = 1153 (318.6 bits), Expect = 6.3e-109, Sum P(2) = 6.3e-109
Identities = 233/236 (98%), Positives = 233/236 (98%), Strand = Plus / Plus

```
Query:  3268 GTGAAACAGGGAGCCACCAAAACTTTGGGGAGCAGGCTAGTGCCGGTTTTGACCACCTGT 3327
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:     1 GTGAAACAGGGAGCCACCAAAACTTTGGGGAGCAGGCTAGTGCCGGTTTTGACCACCTGT 60

Query:  3328 GGAGCAGTGCTCACTCACGAAGGCATTTTGCCATCACATGAATGTGCAGAAAGGAGGCCA 3387
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    61 GGAGCAGTGCTCACTCACGAAGGCATTTTGCCATCACATGAATGTGCAGAAAGGAGGCCA 120

Query:  3388 AAAGCATTCTGTGCTTCTCCACCACAGCACAGACTTCCCTAGTCTCATTTGCTGAGAGTA 3447
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   121 AAAGCATTCTGTGCTTCTCCACCACAGCACAGACTTCCCTAGTCTCATTTGCTGAGAGTA 180

Query:  3448 GACATTCTGAGGGCCAGCAGTGCAGGTGTGATGTGCCTCAGAGGGTATGAAGCCCT 3503
             ||||||||||||||||||||||||||||||||||||||||||||||||||  || |
Sbjct:   181 GACATTCTGAGGGCCAGCAGTGCAGGTGTGATGTGCCTCAGAGGGTATGAGCCCTT 236
```

Score = 320 (88.4 bits), Expect = 6.3e-109, Sum P(2) = 6.3e-109
Identities = 64/64 (100%), Positives = 64/64 (100%), Strand = Plus / Plus

```
Query:  3498 AGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGATATCTAGAAGGCTAATTG 3557
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   230 AGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGATATCTAGAAGGCTAATTG 289

Query:  3558 ATTT 3561
             ||||
Sbjct:   290 ATTT 293
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NCBI **Sequence revision history** Entrez ?

Revision History for Accession = Y07637	
gi	*Update Date*
174370	03/05/97

This sequence was released by NCBI on 12/20/96

Dis[illegible]NT

NCBI Entrez Nucleotide QUERY BLAST Entrez ?

Other Formats: FASTA Graphic

Links: MEDLINE Protein Related Sequences

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LOCUS       HSGABACHL    3153 bp    RNA             PRI       03-MAR-1997
DEFINITION  H.sapiens mRNA for putative GABA-gated chloride channel.
ACCESSION   Y07637
NID         g1747370
KEYWORDS    GABA-gated chloride channel.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3153)
  AUTHORS   Garret,M., Bascles,L., Boue-Grabot,E., Sartor,P., Charron,G.,
            Bloch,B. and Margolskee,R.F.
  TITLE     An mRNA encoding a putative GABA-gated chloride channel is
            expressed in the human cardiac conduction system
  JOURNAL   J. Neurochem. 68, 1382-1389 (1997)
REFERENCE   2  (bases 1 to 3153)
  AUTHORS   Garret,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-AUG-1996) M. Garret, CNRS UMR5543, Laboratoire de
            Neurophysiologie, Universite de Bordeaux2, 146 rue Leo Saignat,
            33076 Bordeaux Cedex, FRANCE
FEATURES             Location/Qualifiers
     source          1..3153
                     /organism="Homo sapiens"
     CDS             51..1568
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                     /codon_start=1
                     /product="putative GABA-gated chloride channel"
                     /db_xref="PID:e274573"
                     /db_xref="PID:g1747371"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIA
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPGDFMVMTIFFNVSRRF
                     GYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVS
                     YITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRAR
                     SRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCK
                     RFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
     polyA_signal    3118..3123
BASE COUNT      726 a    885 c    687 g    855 t
ORIGIN
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       61 aagttcttcc agtcctccta ggcatcttat tgatcctcca gtcgagggtc gagggacctc
      121 agactgaatc aaagaatgaa gcctcttccc gtgatgttgt ctatggcccc cagccccagc
      181 ctctggaaaa tcagctcctc tctgaggaaa caaagtcaac tgagactgag actgggagca
      241 gagttggcaa actgccagaa gcctctcgca tcctgaacac tatcctgagt aattatgacc
      301 acaaactgcg ccctggcatt ggagagaagc ccactgtggt cactgttgag atcgccgtca
      361 acagccttgg tcctctctct atcctagaca tggaatacac cattgacatc atcttctccc
      421 agacctggta cgacgaacgc ctctgttaca acgacacctt tgagtctctt gttctgaatg
      481 gcaatgtggt gagccagcta tggatcccgg acacctttt taggaattct aagaggaccc
      541 acgagcatga gatcaccatg cccaaccaga tggtccgcat ctacaaggat ggcaaggtgt
      601 tgtacacaat taggatgacc attgatgccg gatgctcact ccacatgctc agatttccaa
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Save the above report in Macintosh Text format.

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Length = 3153

Plus Strand HSPs:

Score = 1180 (326.1 bits), Expect = 7.6e-87, P = 7.6e-87
Identities = 236/236 (100%), Positives = 236/236 (100%), Strand = Plus / Plus

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NCBI **Sequence revision history** Entrez ?

Revision History for Accession = U66661	
gi	*Update Date*
1857125	03/11/97

This sequence was released by NCBI on 03/04/97

Disclaimer

NCBI Entrez Nucleotide QUERY BLAST Entrez ?

Other Formats: FASTA Graphic

Links: MEDLINE Protein Related Sequences

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LOCUS       HSU66661     3154 bp    mRNA            PRI       11-MAR-1997
DEFINITION  Human GABA-A receptor epsilon subunit mRNA, complete cds.
ACCESSION   U66661
NID         g1857125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3154)
  AUTHORS   Davies,P.A., Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Insensitivity to anaesthetic agents conferred by a class of GABA(A)
            receptor subunit
  JOURNAL   Nature 385 (6619), 820-823 (1997)
  MEDLINE   97192095
REFERENCE   2  (bases 1 to 3154)
  AUTHORS   Davies,P.A., Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-AUG-1996) Department of Cellular and Molecular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
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Length = 3154

Plus Strand HSPs:

Score = 1170 (323.3 bits), Expect = 5.2e-86, P = 5.2e-86
Identities = 234/234 (100%), Positives = 234/234 (100%), Strand = Plus / Plus

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NCBI Entrez Nucleotide QUERY BLAST Entrez ?

Other Formats: FASTA | Graphic

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DEFINITION  Human GABA-A receptor epsilon subunit (GABRE) gene, exon 1.
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NID         g2735345
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
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            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 556)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
            epsilon subunit on chromosome Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 556)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-1997) Department of Molecular and Cellular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
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NCBI **Sequence revision history** Entrez ?

Revision History for Accession = U92281	
gi	*Update Date*
2733345	01/03/98

This sequence was released by NCBI on 01/01/98

Disclaimer

NCBI Entrez **Nucleotide QUERY** BLAST Entrez ?

Other Formats: FASTA Graphic

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LOCUS       HSGABRE2     1097 bp    DNA             PRI       03-JAN-1998
DEFINITION  Human GABA-A receptor epsilon subunit (GABRE) gene, exons 2 and 3.
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NID         g2735346
KEYWORDS    .
SOURCE      human.
  ORGANISM  [illegible]
            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1097)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
            epsilon subunit on chromosome Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1097)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-1997) Department of Molecular and Cellular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
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Save the above report in Macintosh Text format

NCBI **Sequence revision history** Entrez ?

Revision History for Accession = U92282	
gi	*Update Date*
2755346	01/03/98

This sequence was released by NCBI on 01/01/98

NCBI Entrez **Nucleotide QUERY** BLAST Entrez2 ?!

Other Formats: FASTA | Graphic

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DEFINITION  Human GABA-A receptor epsilon subunit (GABRE) gene, exons 4-9, and
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NID         g2735347
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SOURCE      human.
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 9631)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
            epsilon subunit on chromosome Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 9631)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-1997) Department of Molecular and Cellular
            Biology, The Institute for Genomic Research, 9712 Medical Center
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Save the above report in Macintosh Text format

NCBI **Sequence revision history** Entrez ?

Revision History for Accession = U92283	
gi	***Update Date***
1735347	01/03/98

This sequence was released by NCBI on 01/01/98

Disclaimer

NCBI Entrez **Nucleotide QUERY** BLAST Entrez ?

Other Formats: FASTA Graphic

Links: Protein

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NID         g2735328
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  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
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  JOURNAL   Unpublished
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  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-1997) Department of Molecular and Cellular
            Biology, The Institute for Genomic Research, 9712 Medical Center
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Other Formats: FASTA | Graphic

Links: Related Sequences

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  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
            epsilon subunit on chromosome Xq28
  JOURNAL   Unpublished
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  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-1997) Department of Molecular and Cellular
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Revision History for Accession = U92285	
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This sequence was released by NCBI on 01/01/98

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NCBI Entrez Nucleotide QUERY BLAST Entrez ?

Other Formats: FASTA | Graphic

Links: MEDLINE | Related Sequences

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ACCESSION   Y09764
NID         g2285959
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SOURCE      human.
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  AUTHORS   Wilke,K., Gaul,R., Klauck,S.M. and Poustka,A.
  TITLE     A gene in human chromosome band Xq28 (GABRE) defines a putative new
            subunit class of the GABAA neurotransmitter receptor
  JOURNAL   Genomics 45 (1), 1-10 (1997)
  MEDLINE   97480709
REFERENCE   2  (bases 1 to 10897)
  AUTHORS   Wilke,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-1996) K. Wilke, Deutsches Krebsforschungszentrum,
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Revision History for Accession = Y09764	
gi	***Update Date***
2285959	11/02/97

This sequence was released by NCBI on 07/30/97

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NCBI Entrez **Nucleotide QUERY** BLAST Entrez ?

Other Formats: FASTA | Graphic

Links: MEDLINE | Protein | Related Sequences

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LOCUS       HSY09765     3150 bp    RNA             PRI       31-OCT-1997
DEFINITION  Homo sapiens mRNA for putative GABA receptor epsilon subunit.
ACCESSION   Y09765
NID         g2285960
KEYWORDS    GABA receptor; GABRE gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3150)
  AUTHORS   Wilke,K., Gaul,R., Klauck,S.M. and Poustka,A.
  TITLE     A gene in human chromosome band Xq28 (GABRE) defines a putative new
            subunit class of the GABAA neurotransmitter receptor
  JOURNAL   Genomics 45 (1), 1-10 (1997)
  MEDLINE   97480709
REFERENCE   2  (bases 1 to 3150)
  AUTHORS   Wilke,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-1996) K. Wilke, Deutsches Krebsforschungszentrum,
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            D-69120 Heidelberg, FRG
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Revision History for Accession = Y09765	
gi	*Update Date*
2285960	11/02/97

This sequence was released by NCBI on 07/30/97

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